

(1) GENERAL INFORMATION

- (2) INFORMATION FOR SEQ ID NO:1:

- SUBSTITUTE SHEET (RULE 26)**

28

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

23

CGGCTACTAG TGCAGTTCTT GAA

(2) INFORMATION FOR SEQ ID NO:3:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

29

ATCGTACTAG T.GAG.CCA. GTA.GAT.C

(2) INFORMATION FOR SEQ ID NO:4:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

24

CGGCTACTAG TTTCCTTCGG GCCT

(2) INFORMATION FOR SEQ ID NO:5:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

23

ATCGTCCATG GAGCCAGTAG ATC

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATGGATCCAA	AAACTTTAGC	CCTTTCTTTA	TTAGCAGCTG	GCGTACTAGC	AGGTTGTAGC	60
AGCCATTTCAT	CAAATATGGC	GAATACCCAA	ATGAAATCAG	ACAAAATCAT	TATTGCTCAC	120
CGTGGTGCTA	GCGGTTATTT	ACCAGAGCAT	ACGTTAGAAT	CTAAAGCACT	TGCTTTTGCA	180
CAACAGGCTG	ATTATTTAGA	GCAAGATTTA	GCAATGACTA	AGGATGGTCG	TTTAGTGGTT	240
ATTCACGATC	ACTTTT TAGA	TGGCTTGACT	GATGTTGCGA	AAAAATTCCT	ACATCGTCAT	300
CGTAAAGATG	GCCGTTACTA	TGTCATCGAC	TTTACCTTAA	AAGAAATTCA	AAGTTTAGAA	360
ATGACAGAAA	ACTTTGAAAC	CATGGCCACG	TGTGATCAGA	GCTCAACTAG	TGGCCACCAT	420
CACCATCACC	ATTAATCTAG	A				441

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Asp	Pro	Lys	Thr	Leu	Ala	Leu	Ser	Leu	Leu	Ala	Ala	Gly	Val	Leu	1	5	10	15
Ala	Gly	Cys	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys	20	25	30	
Ser	Asp	Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro	35	40	45	
Glu	His	Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp	50	55	60	
Tyr	Leu	Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val	65	70	75	80
Ile	His	Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe	85	90	95	
Pro	His	Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr	100	105	110	
Leu	Lys	Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met	115	120	125	
Ala	Thr	Cys	Asp	Gln	Ser	Ser	Thr	Ser	Gly	His	His	His	His	His	His	130	135	140	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 648 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ATGGGTGGCA	AGTGGTCAAA	AAGTAGTGTG	GTTGGATGGC	CTACTGTAAG	GGAAAAGTATG	60
AGACGAGCTG	AGCCAGCAGC	AGATGGGGTG	GGAGCAGCAT	CTCGAGACCT	GGAAAAACAT	120
GGAGCAATCA	CAAGTAGCAA	TACAGCAGCT	ACCAATGCTG	CTTGTGCCTG	GCTAGAAGCA	180
CAAGAGGAGG	AGGAGGTGGG	TTTTCCAGTC	ACACCTCAGG	TACCTTTAAG	ACCAATGACT	240
TACAAGGCAG	CTGTAGATCT	TAGCCACTTT	TTAAAAGAAA	AGGGGGGACT	GGAAGGGCTA	300
ATTCAC TCCC	AACGAAGACA	AGATATCCTT	GATCTGTGGA	TCTACCACAC	ACAAGGCTAC	360
TTCCCTGATT	GGCAGAACTA	CACACCAGGG	CCAGGGGGTCA	GATATCCACT	GACCTTTTGA	420
TGGTGCTACA	AGCTAGTACC	AGTTGAGCCA	GATAAGGTTAG	AAGAGGCCAA	TAAAGGAGAG	480
AACACCAGCT	TGTTACACCC	TGTGAGCCCTG	CATGGAATGG	ATGACCCTGA	GAGAGAAGTG	540
TTAGAGTGGA	GGTTTGACAG	CCGCCTAGCA	TTTCATCACG	TGGCCCGAGA	GCTGCATCCG	600
GAGTACTTCA	AGAACTGCAC	TAGTGGCCAC	CATCACCATC	ACCATTAA		648

(A) LENGTH: 216 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met 1	Gly	Gly	Lys	Trp 5	Ser	Lys	Ser	Ser	Val 10	Val	Gly	Trp	Pro	Thr 15	Val
Arg	Glu	Arg	Met 20	Arg	Arg	Ala	Glu	Pro 25	Ala	Ala	Asp	Gly	Val 30	Gly	Ala
Ala	Ser	Arg	Asp 35	Leu	Glu	Lys	His 40	Gly	Ala	Ile	Thr	Ser 45	Ser	Asn	Thr
Ala	Ala 50	Thr	Asn	Ala	Ala	Cys 55	Ala	Trp	Leu	Glu	Ala 60	Gln	Glu	Glu	Glu
Glu 65	Val	Gly	Phe	Pro	Val 70	Thr	Pro	Gln	Val	Pro 75	Leu	Arg	Pro	Met	Thr 80
Tyr	Lys	Ala	Ala 85	Val	Asp	Leu	Ser	His 90	Phe	Leu	Lys	Glu	Lys	Gly 95	Gly
Leu	Glu	Gly	Leu 100	Ile	His	Ser	Gln	Arg 105	Arg	Gln	Asp	Ile	Leu 110	Asp	Leu
Trp	Ile	Tyr 115	His	Thr	Gln	Gly	Tyr 120	Phe	Pro	Asp	Trp	Gln 125	Asn	Tyr	Thr
Pro	Gly 130	Pro	Gly	Val	Arg	Tyr 135	Pro	Leu	Thr	Phe	Gly 140	Trp	Cys	Tyr	Lys
Leu 145	Val	Pro	Val	Glu	Pro 150	Asp	Lys	Val	Glu	Glu 155	Ala	Asn	Lys	Gly	Glu 160
Asn	Thr	Ser	Leu 165	Leu	His	Pro	Val	Ser	Leu 170	His	Gly	Met	Asp	Asp 175	Pro
Glu	Arg	Glu	Val 180	Leu	Glu	Trp	Arg	Phe 185	Asp	Ser	Arg	Leu	Ala 190	Phe	His
His	Val	Ala 195	Arg	Glu	Leu	His	Pro 200	Glu	Tyr	Phe	Lys	Asn 205	Cys	Thr	Ser
Gly	His 210	His	His	His	His	His	His 215								

SUBSTITUTE SHEET (RULE 26)

(A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGAGCCAG	TAGATCCTAG	ACTAGAGCCC	TGGAAGCATC	CAGGAAGTCA	GCCTAAAACT	60
GCTTGTACCA	ATTGCTATTG	TAAAAAGTGT	TGCTTTCATT	GCCAAGTTTG	TTTCATAACA	120
AAAGCCTTAG	GCATCTCCTA	TGGCAGGAAG	AAGCGGAGAC	AGCGACGAAG	ACCTCCTCAA	180
GGCAGTCAGA	CTCATCAAGT	TTCTCTATCA	AAGCAACCCA	CCTCCCAATC	CCGAGGGGAC	240
CCGACAGGCC	CGAAGGAAAC	TAGTGGCCAC	CATCACCATC	ACCATTAA		288

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(A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
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Met	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
1				5					10					15	
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
			20					25					30		
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly
		35				40					45				
Arg	Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr
	50				55						60				
His	Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp
65				70					75						80
Pro	Thr	Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His	
			85					90						95	

(A) LENGTH: 909 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGGTGGCA	AGTGGTCAAA	AAGTAGTGTG	GTTGGATGGC	CTACTGTAAG	GGAAAGAATG	60
AGACGAGCTG	AGCCAGCAGC	AGATGGGGTG	GGAGCAGCAT	CTCGAGACCT	GGAAAAACAT	120
GGAGCAATCA	CAAGTAGCAA	TACAGCAGCT	ACCAATGCTG	CTTGTGCCTG	GCTAGAAAGCA	180
CAAGAGGAGG	AGGAGGTGGG	TTTTCCAGTC	ACACCTCAGG	TACCTTTAAG	ACCAATGACT	240
TACAAGGCAG	CTGTAGATCT	TAGCCACTTT	TTAAAAGAAA	AGGGGGGACT	GGAAAGGGCTA	300
ATTCACCTCC	AACGAAGACA	AGATATCCTT	GATCTGTGGA	TCTACCACAC	ACAAGGCTAC	360

(2) INFORMATION FOR SEQ ID NO:13:

(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met 1	Gly	Gly	Lys	Trp 5	Ser	Lys	Ser	Ser	Val 10	Val	Gly	Trp	Pro 15	Val	
Arg	Glu	Arg	Met 20	Arg	Arg	Ala	Glu	Pro 25	Ala	Ala	Asp	Gly	Val 30	Gly	Ala
Ala	Ser	Arg	Asp 35	Leu	Glu	Lys	His 40	Gly	Ala	Ile	Thr	Ser 45	Ser	Asn	Thr
Ala	Ala	Thr	Asn 50	Ala	Ala	Cys 55	Ala	Trp	Leu	Glu	Ala 60	Gln	Glu	Glu	Glu
Glu 65	Val	Gly	Phe 70	Pro	Val	Thr	Pro	Gln	Val 75	Pro	Leu	Arg	Pro	Met	Thr 80
Tyr	Lys	Ala	Ala 85	Val	Asp	Leu	Ser	His 90	Phe	Leu	Lys	Glu	Lys	Gly 95	Gly
Leu	Glu	Gly	Leu 100	Ile	His	Ser	Gln	Arg 105	Arg	Gln	Asp	Ile	Leu	Asp	Leu
Trp	Ile	Tyr 115	His	Thr	Gln	Gly	Tyr 120	Phe	Pro	Asp	Trp	Gln 125	Asn	Tyr	Thr
Pro	Gly 130	Pro	Gly	Val	Arg	Tyr 135	Pro	Leu	Thr	Phe	Gly 140	Trp	Cys	Tyr	Lys
Leu 145	Val	Pro	Val	Glu	Pro	Asp 150	Lys	Val	Glu	Glu	Ala 155	Asn	Lys	Gly	Glu 160
Asn	Thr	Ser	Leu 165	Leu	His	Pro	Val	Ser 170	Leu	His	Gly	Met	Asp	Asp 175	Pro
Glu	Arg	Glu	Val 180	Leu	Glu	Trp	Arg	Phe 185	Asp	Ser	Arg	Leu	Ala 190	Phe	His
His	Val 195	Ala	Arg	Glu	Leu	His	Pro 200	Glu	Tyr	Phe	Lys	Asn 205	Cys	Thr	Ser
Glu	Pro 210	Val	Asp	Pro	Arg	Leu 215	Glu	Pro	Trp	Lys	His 220	Pro	Gly	Ser	Gln
Pro 225	Lys	Thr	Ala	Cys	Thr	Asn 230	Cys	Tyr	Cys	Lys 235	Lys	Cys	Cys	Phe	His 240
Cys	Gln	Val	Cys 245	Phe	Ile	Thr	Lys	Ala	Leu 250	Gly	Ile	Ser	Tyr	Gly 255	Arg
Lys	Lys	Arg	Arg 260	Gln	Arg	Arg	Arg	Pro 265	Pro	Gln	Gly	Ser	Gln 270	Thr	His
Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro

(2) INFORMATION FOR SEQ ID NO:14:

(A) LENGTH: 1029 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGATCCAA	AAACTTTAGC	CCTTTCTTTA	TTAGCAGCTG	GCGTACTAGC	AGGTTGTAGC	60
AGCCATTCAT	CAAATATGGC	GAATACCCAA	ATGAAATCAG	ACAAAATCAT	TATTGCTCAC	120
CGTGGTGCTA	GCGGTTATTT	ACCAGAGCAT	ACGTTAGAAT	CTAAAGCACT	TGCTTTTGCA	180
CAACAGGCTG	ATTATTTAGA	GCAAGATTTA	GCAATGACTA	AGGATGGTCG	TTTAGTGGTT	240
ATTACGATC	ACTTTT TAGA	TGGCTTGACT	GATGTTGCGA	AAAAATTCCC	ACATCGTCAT	300
CGTAAAGATG	GCCGTTACTA	TGTCATCGAC	TTTACCTTAA	AAGAAATTCA	AAGTTTAGAA	360
ATGACAGAAA	ACTTTGAAAC	CATGGGTGGC	AAGTGGTCAA	AAAGTAGTGT	GGTTGGATGG	420
CCTACTGTAA	GGGAAAGAAT	GAGACGAGCT	GAGCCAGCAG	CAGATGGGGT	GGGAGCAGCA	480
TCTCGAGACC	TGGAAAAACA	TGGAGCAATC	ACAAGTAGCA	ATACAGCAGC	TACCAATGCT	540
GCTTGTGCCT	GGCTAGAAGC	ACAAGAGGAG	GAGGAGGTGG	GTTTTCCAGT	CACACCTCAG	600
GTACCTTTAA	GACCAATGAC	TTACAAGGCA	GCTGTAGATC	TTAGCCACTT	TTTAAAAGAA	660
AAGGGGGGAC	TGGAAGGGCT	AATTCACTCC	CAACGAAGAC	AAGATATCCT	TGATCTGTGG	720
ATCTACCACA	CACAAGGCTA	CTTCCCTGAT	TGGCAGAACT	ACACACCAGG	GCCAGGGGTC	780
AGATATCCAC	TGACCTTTGG	ATGGTGCTAC	AAGCTAGTAC	CAGTTGAGCC	AGATAAGGTA	840
GAAGAGGCCA	ATAAAGGAGA	GAACACCAGC	TTGTTACACC	CTGTGAGCCT	GCATGGAATG	900
GATGACCCTG	AGAGAGAAGT	GTTAGAGTGG	AGGTTTGACA	GCCGCCTAGC	ATTTTCATCAC	960
GTGGCCCCGAG	AGCTGCATCC	GGAGTACTTC	AAGAACTGCA	CTAGTGGCCA	CCATCACCAT	1020
CACCATTAA						1029

(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Cys 1	Ser	Ser	His	Ser 5	Ser	Asn	Met	Ala	Asn 10	Thr	Gln	Met	Lys	Ser 15	Asp
Lys	Ile	Ile	Ile	Ala 20	His	Arg	Gly	Ala 25	Ser	Gly	Tyr	Leu	Pro 30	Glu	His
Thr	Leu	Glu 35	Ser	Lys	Ala	Leu	Ala 40	Phe	Ala	Gln	Gln	Ala 45	Asp	Tyr	Leu
Glu	Gln 50	Asp	Leu	Ala	Met	Thr 55	Lys	Asp	Gly	Arg	Leu 60	Val	Val	Ile	His
Asp 65	His	Phe	Leu	Asp	Gly 70	Leu	Thr	Asp	Val	Ala 75	Lys	Lys	Phe	Pro	His 80
Arg	His	Arg	Lys	Asp 85	Gly	Arg	Tyr	Tyr	Val 90	Ile	Asp	Phe	Thr	Leu 95	Lys

Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met Gly Gly
 100 105 110
 Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg Glu Arg
 115 120 125
 Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala Ser Arg
 130 135 140
 Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala Ala Thr
 145 150 155 160
 Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Val Gly
 165 170 175
 Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr Lys Ala
 180 185 190
 Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu Glu Gly
 195 200 205
 Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp Ile Tyr
 210 215 220
 His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro Gly Pro
 225 230 235 240
 Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu Val Pro
 245 250 255
 Val Glu Pro Asp Lys Val Glu Glu Ala Asn Lys Gly Glu Asn Thr Ser
 260 265 270
 Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu Arg Glu
 275 280 285
 Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His Val Ala
 290 295 300
 Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Gly His His
 305 310 315 320
 His His His His

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGATCCAA	AAACTTTAGC	CCTTTCTTTA	TTAGCAGCTG	GCGTACTAGC	AGGTTGTAGC	60
AGCCATTTCAT	CAAATATGGC	GAATACCCAA	ATGAAATCAG	ACAAAATCAT	TATTGCTCAC	120
CGTGGTGCTA	GCGGTTATTT	ACCAGAGCAT	ACGTTAGAAT	CTAAAGCACT	TGCGTTTGCA	180
CAACAGGCTG	ATTATTTAGA	GCAAGATTTA	GCAATGACTA	AGGATGGTCG	TTTAGTTGGTT	240
ATTCACGATC	ACTTTTTAGA	TGGCTTGACT	GATGTTGCGA	AAAAATTCCC	ACATCGTCAT	300
CGTAAAGATG	GCCGTTACTA	TGTCATCGAC	TTTACCTTAA	AAGAAATTCA	AAGTTTAGAA	360
ATGACAGAAA	ACTTTGAAAC	CATGGGTGGC	AAGTGGTCAA	AAAGTAGTGT	GGTTGGATGG	420
CCTACTGTAA	GGGAAAGAAT	GAGACGAGCT	GAGCCAGCAG	CAGATGGGGT	GGGAGCAGCA	480
TCTCGAGACC	TGGAAAAACA	TGGAGCAATC	ACAAGTAGCA	ATACAGCAGC	TACCAATGCT	540
GCTTGTGCCT	GGCTAGAAGC	ACAAGAGGAG	GAGGAGGTGG	GTTTTCCAGT	CACACCTCAG	600
GTACCTTTAA	GACCAATGAC	TTACAAGGCA	GCTGTAGATC	TTAGCCACTT	TTTAAAGAA	660
AAGGGGGGAC	TGGAAGGGCT	AATTCACCTC	CAACGAAGAC	AAGATATCCT	TGATCTGTGG	720
ATCTACCACA	CACAAGGCTA	CTTCCCTGAT	TGGCAGAACT	ACACACCAGG	GCCAGGGGTC	780
AGATATCCAC	TGACCTTTGG	ATGGTGCTAC	AAGCTAGTAC	CAGTTGAGCC	AGATAAGGTA	840
GAAGAGGCCA	ATAAAGGAGA	GAACACCAGC	TTGTTACACC	CTGTGAGCCT	GCATGGAATG	900

GATGACCCTG	AGAGAGAAGT	GTTAGAGTGG	AGGTTTGACA	GCCGCCTAGC	ATTTCATCAC	960
GTGGCCCGAG	AGCTGCATCC	GGAGTACTTC	AAGAACTGCA	CTAGTGAGCC	AGTAGATCCT	1020
AGACTAGAGC	CCTGGAAGCA	TCCAGGAAGT	CAGCCTAAAA	CTGCTTGATC	CAATTGCTAT	1080
TGTAAAAAGT	GTTGCTTTCA	TTGCCAAGTT	TGTTTCATAA	CAAAAGCCTT	AGGCATCTCC	1140
TATGGCAGGA	AGAAGCGGAG	ACAGCGACGA	AGACCTCCTC	AAGGCAGTCA	GACTCATCAA	1200
GTTTCTCTAT	CAAAGCAACC	CACCTCCCAA	TCCCGAGGGG	ACCCGACAGG	CCCGAAGGAA	1260
ACTAGTGGCC	ACCATCACCA	TCACCATTAA				1290

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Cys	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys	Ser	Asp	1	5	10	15
Lys	Ile	Ile	Ile	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Leu	Pro	Glu	His	20	25	30	
Thr	Leu	Glu	Ser	Lys	Ala	Leu	Ala	Phe	Ala	Gln	Gln	Ala	Asp	Tyr	Leu	35	40	45	
Glu	Gln	Asp	Leu	Ala	Met	Thr	Lys	Asp	Gly	Arg	Leu	Val	Val	Ile	His	50	55	60	
Asp	His	Phe	Leu	Asp	Gly	Leu	Thr	Asp	Val	Ala	Lys	Lys	Phe	Pro	His	65	70	75	80
Arg	His	Arg	Lys	Asp	Gly	Arg	Tyr	Tyr	Val	Ile	Asp	Phe	Thr	Leu	Lys	85	90	95	
Glu	Ile	Gln	Ser	Leu	Glu	Met	Thr	Glu	Asn	Phe	Glu	Thr	Met	Gly	Gly	100	105	110	
Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val	Arg	Glu	Arg	115	120	125	
Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala	Ala	Ser	Arg	130	135	140	
Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr	Ala	Ala	Thr	145	150	155	160
Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu	Glu	Val	Gly	165	170	175	
Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr	Tyr	Lys	Ala	180	185	190	
Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly	Leu	Glu	Gly	195	200	205	
Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu	Trp	Ile	Tyr	210	215	220	
His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro	Gly	Pro	225	230	235	240
Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	Val	Pro	245	250	255	
Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	Thr	Ser	260	265	270	
Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	Arg	Glu	275	280	285	
Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His	His	Val	Ala	290	295	300	

10 / 15

Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Glu Pro Val
 305 310 315 320
 Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser Gln Pro Lys Thr
 325 330 335
 Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe His Cys Gln Val
 340 345 350
 Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly Arg Lys Lys Arg
 355 360 365
 Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr His Gln Val Ser
 370 375 380
 Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp Pro Thr Gly Pro
 385 390 395 400
 Lys Glu Thr Ser Gly His His His His His His
 405 410

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 981 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAAATC	60
ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA	120
CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT	180
CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC	240
CCACATCGTC	ATCGTAAAGA	TGGCCGTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT	300
CAAAGTTTAG	AAATGACAGA	AAACTTTGAA	ACCATGGGTG	GCAAGTGGTC	AAAAAGTAGT	360
GTGGTTGGAT	GGCCTACTGT	AAGGGAAAGA	ATGAGACGAG	CTGAGCCAGC	AGCAGATGGG	420
GTGGGAGCAG	CATCTCGAGA	CCTGGAAAAA	CATGGAGCAA	TCACAAGTAG	CAATACAGCA	480
GCTACCAATG	CTGCTTGTGC	CTGGCTAGAA	GCACAAGAGG	AGGAGGAGGT	GGGTTTTCCA	540
GTCACACCTC	AGGTACCTTT	AAGACCAATG	ACTTACAAGG	CAGCTGTAGA	TCTTAGCCAC	600
TTTTTAAAAG	AAAAGGGGGG	ACTGGAAGGG	CTAATTCACT	CCCAACGAAG	ACAAGATATC	660
CTTGATCTGT	GGATCTACCA	CACACAAGGC	TACTTCCCTG	ATTGGCAGAA	CTACACACCA	720
GGGCCAGGGG	TCAGATATCC	ACTGACCTTT	GGATGGTGCT	ACAAGCTAGT	ACCAGTTGAG	780
CCAGATAAGG	TAGAAGAGGC	CAATAAAGGA	GAGAACACCA	GCTTGTTACA	CCCTGTGAGC	840
CTGCATGGAA	TGGATGACCC	TGAGAGAGAA	GTGTTAGAGT	GGAGGTTTGA	CAGCCGCCTA	900
GCATTTTCATC	ACGTGGCCCCG	AGAGCTGCAT	CCGGAGTACT	TCAAGAACTG	CACTAGTGGC	960
CACCATCACC	ATCACCATTA	A				981

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met	Asp	Pro	Ser	Ser	His	Ser	Ser	Asn	Met	Ala	Asn	Thr	Gln	Met	Lys
1				5				10					15		

Ser Asp Lys Ile Ile Ile Ala His Arg Gly Ala Ser Gly Tyr Leu Pro
 20 25 30
 Glu His Thr Leu Glu Ser Lys Ala Leu Ala Phe Ala Gln Ala Asp
 35 40 45
 Tyr Leu Glu Gln Asp Leu Ala Met Thr Lys Asp Gly Arg Leu Val Val
 50 55 60
 Ile His Asp His Phe Leu Asp Gly Leu Thr Asp Val Ala Lys Lys Phe
 65 70 75 80
 Pro His Arg His Arg Lys Asp Gly Arg Tyr Tyr Val Ile Asp Phe Thr
 85 90 95
 Leu Lys Glu Ile Gln Ser Leu Glu Met Thr Glu Asn Phe Glu Thr Met
 100 105 110
 Gly Gly Lys Trp Ser Lys Ser Ser Val Val Gly Trp Pro Thr Val Arg
 115 120 125
 Glu Arg Met Arg Arg Ala Glu Pro Ala Ala Asp Gly Val Gly Ala Ala
 130 135 140
 Ser Arg Asp Leu Glu Lys His Gly Ala Ile Thr Ser Ser Asn Thr Ala
 145 150 155 160
 Ala Thr Asn Ala Ala Cys Ala Trp Leu Glu Ala Gln Glu Glu Glu Glu
 165 170 175
 Val Gly Phe Pro Val Thr Pro Gln Val Pro Leu Arg Pro Met Thr Tyr
 180 185 190
 Lys Ala Ala Val Asp Leu Ser His Phe Leu Lys Glu Lys Gly Gly Leu
 195 200 205
 Glu Gly Leu Ile His Ser Gln Arg Arg Gln Asp Ile Leu Asp Leu Trp
 210 215 220
 Ile Tyr His Thr Gln Gly Tyr Phe Pro Asp Trp Gln Asn Tyr Thr Pro
 225 230 235 240
 Gly Pro Gly Val Arg Tyr Pro Leu Thr Phe Gly Trp Cys Tyr Lys Leu
 245 250 255
 Val Pro Val Glu Pro Asp Lys Val Glu Ala Asn Lys Gly Glu Asn
 260 265 270
 Thr Ser Leu Leu His Pro Val Ser Leu His Gly Met Asp Asp Pro Glu
 275 280 285
 Arg Glu Val Leu Glu Trp Arg Phe Asp Ser Arg Leu Ala Phe His His
 290 295 300
 Val Ala Arg Glu Leu His Pro Glu Tyr Phe Lys Asn Cys Thr Ser Gly
 305 310 315 320
 His His His His His His
 325

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGGATCCAA	GCAGCCATTC	ATCAAATATG	GCGAATACCC	AAATGAAATC	AGACAAATC	60
ATTATTGCTC	ACCGTGGTGC	TAGCGGTTAT	TTACCAGAGC	ATACGTTAGA	ATCTAAAGCA	120
CTTGCGTTTG	CACAACAGGC	TGATTATTTA	GAGCAAGATT	TAGCAATGAC	TAAGGATGGT	180
CGTTTAGTGG	TTATTCACGA	TCACTTTTTA	GATGGCTTGA	CTGATGTTGC	GAAAAAATTC	240
CCACATCGTC	ATCGTAAAGA	TGGCCGTTAC	TATGTCATCG	ACTTTACCTT	AAAAGAAATT	300

(2) INFORMATION FOR SEQ ID NO:21:

(A) LENGTH: 414 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met 1	Asp	Pro	Ser	Ser 5	His	Ser	Ser	Asn 10	Met	Ala	Asn	Thr	Gln	Met 15	Lys
Ser	Asp	Lys	Ile 20	Ile	Ile	Ala	His	Arg 25	Gly	Ala	Ser	Gly	Tyr 30	Leu	Pro
Glu	His	Thr 35	Leu	Glu	Ser	Lys	Ala 40	Leu	Ala	Phe	Ala	Gln 45	Gln	Ala	Asp
Tyr	Leu 50	Glu	Gln	Asp	Leu	Ala 55	Met	Thr	Lys	Asp 60	Gly	Arg	Leu	Val	Val
Ile 65	His	Asp	His	Phe 70	Leu	Asp	Gly	Leu	Thr	Asp 75	Val	Ala	Lys	Lys	Phe 80
Pro	His	Arg	His 85	Arg	Lys	Asp	Gly	Arg	Tyr 90	Tyr	Val	Ile	Asp 95	Phe	Thr
Leu	Lys	Glu 100	Ile	Gln	Ser	Leu	Glu 105	Met	Thr	Glu	Asn	Phe 110	Glu	Thr	Met
Gly	Gly 115	Lys	Trp	Ser	Lys	Ser	Ser 120	Val	Val	Gly	Trp 125	Pro	Thr	Val	Arg
Glu 130	Arg	Met	Arg	Arg	Ala	Glu 135	Pro	Ala	Ala	Asp	Gly 140	Val	Gly	Ala	Ala
Ser 145	Arg	Asp	Leu	Glu 150	Lys	His	Gly	Ala	Ile	Thr 155	Ser	Ser	Asn	Thr	Ala 160
Ala	Thr	Asn 165	Ala	Ala	Cys	Ala	Trp	Leu 170	Glu	Ala	Gln	Glu	Glu	Glu	Glu 175
Val	Gly 180	Phe	Pro	Val	Thr	Pro	Gln 185	Val	Pro	Leu	Arg	Pro	Met 190	Thr	Tyr
Lys	Ala 195	Ala	Val	Asp	Leu	Ser	His 200	Phe	Leu	Lys	Glu 205	Lys	Gly	Gly	Leu
Glu 210	Gly	Leu	Ile	His	Ser	Gln 215	Arg	Arg	Gln	Asp	Ile 220	Leu	Asp	Leu	Trp
Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr	Pro

225	230										235					240
Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys	Leu	
				245					250					255		
Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu	Asn	
				260					265					270		
Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro	Glu	
				275					280					285		
Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His	His	
				290					295					300		
Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser	Glu	
				305					310					315		
Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln	Pro	
				325					330					335		
Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His	Cys	
				340					345					350		
Gln	Val	Cys	Phe	Ile	Thr	Lys	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg	Lys	
				355					360					365		
Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His	Gln	
				370					375					380		
Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Arg	Gly	Asp	Pro	Thr	
				385					390					395		
Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His				
				405					410							

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGGAGCCAG	TAGATCCTAG	ACTAGAGCCC	TGGAAGCATC	CAGGAAGTCA	GCCTAAAAC	60
GCTTGTACCA	ATTGCTATTG	TAAAAAGTGT	TGCTTTCATT	GCCAAGTTTG	TTTCATAACA	120
GCTGCCTTAG	GCATCTCCTA	TGGCAGGAAG	AAGCGGAGAC	AGCGACGAAG	ACCTCCTCAA	180
GGCAGTCAGA	CTCATCAAGT	TTCTCTATCA	AAGCAACCCA	CCTCCAATC	CAAAGGGGAG	240
CCGACAGGCC	CGAAGGAAAC	TAGTGGCCAC	CATCACCATC	ACCATTAA		288

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser
1				5					10					15	
Gln	Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe
			20					25					30		
His	Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly

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(2) INFORMATION FOR SEQ ID NO:24:

(A) LENGTH: 909 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

ATGGGTGGCA	AGTGGTCAAA	AAGTAGTGTG	GTTGGATGGC	CTACTGTAAG	GGAAAGAATG	60
AGAGCAGCTG	AGCCAGCAGC	AGATGGGGTG	GGAGCAGCAT	CTCGAGACCT	GGAAAAACAT	120
GGAGCAATCA	CAAGTAGCAA	TACAGCAGCT	ACCAATGCTG	CTTGTGCCTG	GCTAGAAGCA	180
CAAGAGGAGG	AGGAGGTGGG	TTTTCCAGTC	ACACCTCAGG	TACCTTTAAG	ACCAATGACT	240
TACAAGGCAG	CTGTAGATCT	TAGCCACTTT	TTAAAAGAAA	AGGGGGGACT	GGAAGGGCTA	300
ATTCACTCCC	AACGAAGACA	AGATATCCTT	GATCTGTGGA	TCTACCACAC	ACAAGGCTAC	360
TTCCCTGATT	GGCAGAACTA	CACACCAGGG	CCAGGGGTCA	GATATCCACT	GACCTTTGGA	420
TGGTGCTACA	AGCTAGTACC	AGTTGAGCCA	GATAAGGCTAG	AAGAGGCCAA	TAAAGGAGAG	480
AACACCAGCT	TGTTACACCC	TGTTAGCCTG	CATGGAATGG	ATGACCCTGA	GAGAGAAGTG	540
TTAGAGTGGG	GGTTTGACAG	CCGCCTAGCA	TTTCATCACG	TGGCCCGAGA	GCTGCATCCG	600
GAGTACTTCA	AGAACTGCAC	TAGTGAGCCA	GTAGATCCTA	GACTIONAGCC	CTGGAAGCAT	660
CCAGGAAGTC	AGCCTAAAAC	TGCTTGTACC	AATTGCTATT	GTAAAAAGTG	TTGCTTTTCAT	720
TGCCAAGTTT	GTTTCATAAC	AGCTGCCTTA	GGCATCTCCT	ATGGCAGGAA	GAAGCGGAGA	780
CAGCGACGAA	GACCTCCTCA	AGGCAGTCAG	ACTCATCAAG	TTTCTCTATC	AAAGCAACCC	840
ACCTCCCAAT	CCAAAGGGGA	GCCGACAGGC	CCGAAGGAAA	CTAGTGGCCA	CCATCACCAT	900
CACCATTA						909

(2) INFORMATION FOR SEQ ID NO:25:

(A) LENGTH: 303 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met	Gly	Gly	Lys	Trp	Ser	Lys	Ser	Ser	Val	Val	Gly	Trp	Pro	Thr	Val
1				5					10					15	
Arg	Glu	Arg	Met	Arg	Arg	Ala	Glu	Pro	Ala	Ala	Asp	Gly	Val	Gly	Ala
			20					25					30		
Ala	Ser	Arg	Asp	Leu	Glu	Lys	His	Gly	Ala	Ile	Thr	Ser	Ser	Asn	Thr
			35				40					45			
Ala	Ala	Thr	Asn	Ala	Ala	Cys	Ala	Trp	Leu	Glu	Ala	Gln	Glu	Glu	Glu
	50					55					60				
Glu	Val	Gly	Phe	Pro	Val	Thr	Pro	Gln	Val	Pro	Leu	Arg	Pro	Met	Thr
65					70					75					80

Tyr	Lys	Ala	Ala	Val	Asp	Leu	Ser	His	Phe	Leu	Lys	Glu	Lys	Gly	Gly
				85					90					95	
Leu	Glu	Gly	Leu	Ile	His	Ser	Gln	Arg	Arg	Gln	Asp	Ile	Leu	Asp	Leu
			100					105					110		
Trp	Ile	Tyr	His	Thr	Gln	Gly	Tyr	Phe	Pro	Asp	Trp	Gln	Asn	Tyr	Thr
		115					120					125			
Pro	Gly	Pro	Gly	Val	Arg	Tyr	Pro	Leu	Thr	Phe	Gly	Trp	Cys	Tyr	Lys
		130				135					140				
Leu	Val	Pro	Val	Glu	Pro	Asp	Lys	Val	Glu	Glu	Ala	Asn	Lys	Gly	Glu
145						150				155					160
Asn	Thr	Ser	Leu	Leu	His	Pro	Val	Ser	Leu	His	Gly	Met	Asp	Asp	Pro
				165					170					175	
Glu	Arg	Glu	Val	Leu	Glu	Trp	Arg	Phe	Asp	Ser	Arg	Leu	Ala	Phe	His
			180					185					190		
His	Val	Ala	Arg	Glu	Leu	His	Pro	Glu	Tyr	Phe	Lys	Asn	Cys	Thr	Ser
		195					200					205			
Glu	Pro	Val	Asp	Pro	Arg	Leu	Glu	Pro	Trp	Lys	His	Pro	Gly	Ser	Gln
		210				215					220				
Pro	Lys	Thr	Ala	Cys	Thr	Asn	Cys	Tyr	Cys	Lys	Lys	Cys	Cys	Phe	His
225					230					235					240
Cys	Gln	Val	Cys	Phe	Ile	Thr	Ala	Ala	Leu	Gly	Ile	Ser	Tyr	Gly	Arg
				245					250					255	
Lys	Lys	Arg	Arg	Gln	Arg	Arg	Arg	Pro	Pro	Gln	Gly	Ser	Gln	Thr	His
			260					265					270		
Gln	Val	Ser	Leu	Ser	Lys	Gln	Pro	Thr	Ser	Gln	Ser	Lys	Gly	Glu	Pro
		275					280					285			
Thr	Gly	Pro	Lys	Glu	Thr	Ser	Gly	His	His	His	His	His	His		
	290					295						300			

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTGAAACCA TGGCCGCGGA CTAGTGGCCA CCATCACCAT CACCATTAAC GGAATTC

57

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Thr Ser Gly His His His His His His
1 5